WHAT IS CLAIMED IS:

1. A method of determining whether a subject is at risk for attention deficit hyperactivity disorder (ADHD), wherein said method comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a first group consisting of *TPH, PNMT, ADOA2A, NOS3* and *NAT1*, wherein the presence of said non-wild-type allele of said gene indicates an increased risk of said subject having ADHD as compared to a person with a wild-type allele of each of said genes.

2. The method of claim 1, wherein said method comprises determining for each of said genes whether a non-wild-type allele is present.

3. The method of claim 1, wherein the presence of more than one of said genes comprising a non-wild-type allele indicates a greater risk for ADHD.

4. The method of claim 1, wherein said method further comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a second group consisting of *ADRA2A, ADRA2C, NET, COMT* and *CHRNA4*, wherein the presence of said non-wild-type allele of said gene from said second group indicates an increased risk of said subject having ADHD as compared to a person with a wild-type allele of each of said genes from said second group.

5. The method of claim 4, wherein said method comprises determining for each of said genes of said second group whether a non-wild-type allele is present.

6. The method of claim 4, wherein said method comprises determining for each of said genes of said first group whether a non-wild-type allele is present.

7. The method of claim 4, wherein said method comprises determining for each of said genes of said first group and for each of said genes of said second group whether a non-wild-type allele is present.

8. The method of claim 4, wherein the presence of more than one non-wild-type allele indicates a greater risk for ADHD.

9. A method for developing a polygenic assay that is diagnostic for attention deficit hyperactivity disorder, comprising the steps of:

(a) identifying a trait that is to be studied;

(b) creating a scale measuring the severity of the trait to be studied;

(c) selecting at least one candidate gene that may contribute to said trait, wherein said gene is selected from the group consisting of *TPH, PNMT, ADOA2A, NOS3* and *NAT1*;

(d) identifying at least one polymorphism associated with said candidate gene; and

(e) correlating allelic patterns of said polymorphism with said scale;

wherein allelic patterns that are positively associated with said trait are added, to form a polygenic assay that is diagnostic.

10. A method of determining a treatment modality for a human subject suspected of having attention deficit hyperactivity disorder (ADHD), wherein said method comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a first group consisting of *TPH, PNMT, ADOA2A, NOS3* and *NAT1*, wherein said treatment modality is based upon which of said genes are non-wild-type.

11. The method of claim 10, wherein said method comprises determining for each of said genes whether a non-wild-type allele is present.

12. The method of claim 10, wherein said method further comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a second group consisting of *ADRA2A, ADRA2C, NET, COMT* and *CHRNA4*.

13. The method of claim 12, wherein said method comprises determining for each of said genes of said second group whether a non-wild-type allele is present.

14. The method of claim 12, wherein said method comprises determining for each of said genes of said first group whether a non-wild-type allele is present.

15. The method of claim 12, wherein said method comprises determining for each of said genes of said first group and for each of said genes of said second group whether a non-wild-type allele is present.

16. A method of determining whether a subject is at risk for oppositional defiant disorder (ODD), wherein said method comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a first group consisting of *HTR2A*, *PNMT* and *CD8*, wherein the presence of said non-wild-type allele of said gene indicates an increased risk of said subject having ODD as compared to a person with a wild-type allele of each of said genes.

17. The method of claim 16, wherein said method comprises determining for each of said genes whether a non-wild-type allele is present.

18. The method of claim 16, wherein the presence of more than one of said genes comprising a non-wild-type allele indicates a greater risk for ODD.

19. The method of claim 16, wherein said method further comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a second group consisting of *ADRA2A, ADRA2C, COMT, CHRNA4, NMDAR1* and *CYP*, wherein the presence of said non-wild-type allele of said gene from said second group indicates an increased risk of said subject having ODD as compared to a person with a wild-type allele of each of said genes.

20. The method of claim 19, wherein said method comprises determining for each of said genes of said second group whether a non-wild-type allele is present.

21. The method of claim 19, wherein said method comprises determining for each of said genes of said first group whether a non-wild-type allele is present.

22. The method of claim 19, wherein said method comprises determining for each of said genes of said first group and for each of said genes of said second group whether a non-wild-type allele is present.

23. The method of claim 19, wherein the presence of more than one non-wild-type allele indicates a greater risk for ODD.

24. A method for developing a polygenic assay that is diagnostic for oppositional defiant disorder, comprising the steps of:

(a)identifying the trait that is to be studied;

(b) creating a scale measuring the severity of the trait to be studied;

(c) selecting at least one candidate gene that may contribute to said trait, wherein said gene is selected from the group consisting of *HTR2A*, *PNMT* and *CD8*;

(d) identifying at least one polymorphism associated with said candidate gene; and

(e) correlating allelic patterns of said polymorphism with said scale;

wherein allelic patterns that are positively associated with said trait are added, to form a polygenic assay that is diagnostic.

25. A method of determining a treatment modality for a human subject suspected of having oppositional defiant disorder (ODD), wherein said method comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a first group consisting of *HTR2A*, *PNMT* and *CD8*, wherein said treatment modality is based upon which of said genes are non-wild-type.

26. The method of claim 25, wherein said method comprises determining for each of said genes whether a non-wild-type allele is present.

27. The method of claim 25, wherein said method further comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a second group consisting of *ADRA2A, ADRA2C, COMT, CHRNA4, NMDAR1* and *CYP*.

28. The method of claim 27, wherein said method comprises determining for each of said genes of said second group whether a non-wild-type allele is present.

29. The method of claim 27, wherein said method comprises determining for each of said genes of said first group whether a non-wild-type allele is present.

30. The method of claim 27, wherein said method comprises determining for each of said genes of said first group and for each of said genes of said second group whether a non-wild-type allele is present.

31. A method of determining whether a subject is at risk for conduct disorder (CD), wherein said method comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a first group consisting of *HTR2A, GABBR1, ADOA2A, GRIN2B, NAT1, CCK, CYP, ESR* and *CD8*, wherein the presence of said non-wild-type allele of said gene indicates an increased risk of said subject having CD as compared to a person with a wild-type allele of each of said genes.

32. The method of claim 31, wherein said method comprises determining for each of said genes whether a non-wild-type allele is present.

33. The method of claim 31, wherein the presence of more than one of said genes comprising a non-wild-type allele indicates a greater risk for CD.

34. The method of claim 31, wherein said method further comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a second group consisting of *ADRA2C* and *PSI*, wherein the presence of said non-wild-type allele of said

gene from said second group indicates an increased risk of said subject having CD as compared to a person with a wild-type allele of each of said genes.

35. The method of claim 34, wherein said method comprises determining for each of said genes of said second group whether a non-wild-type allele is present.

36. The method of claim 34, wherein said method comprises determining for each of said genes of said first group whether a non-wild-type allele is present.

37. The method of claim 34, wherein said method comprises determining for each of said genes of said first group and for each of said genes of said second group whether a non-wild-type allele is present.

38. The method of claim 34, wherein the presence of more than one non-wild-type allele indicates a greater risk for CD.

39. A method for developing a polygenic assay that is diagnostic for conduct disorder, comprising the steps of:

(a)identifying the trait that is to be studied;

(b) creating a scale measuring the severity of the trait to be studied;

(c) selecting at least one candidate gene that may contribute to said trait, wherein said gene is selected from the group consisting of *HTR2A, GABBR1, ADOA2A, GRIN2B, NAT1, CCK, CYP, ESR* and *CD8*;

(d) identifying at least one polymorphism associated with said candidate gene; and

(e) correlating allelic patterns of said polymorphism with said scale;

wherein allelic patterns that are positively associated with said trait are added, to form a polygenic assay that is diagnostic.

40. A method of determining a treatment modality for a human subject suspected of having conduct disorder (CD), wherein said method comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a first group

consisting of *HTR2A, GABBR1, ADOA2A, GRIN2B, NAT1, CCK, CYP, ESR* and *CD8*, wherein said treatment modality is based upon which of said genes are non-wild-type.

41. The method of claim 40, wherein said method comprises determining for each of said genes whether a non-wild-type allele is present.

42. The method of claim 40, wherein said method further comprises determining whether said subject's genome comprises a non-wild-type allele of at least one gene selected from a second group consisting of *ADRA2C* and *PSI*.

43. The method of claim 42, wherein said method comprises determining for each of said genes of said second group whether a non-wild-type allele is present.

44. The method of claim 42, wherein said method comprises determining for each of said genes of said first group whether a non-wild-type allele is present.

45. The method of claim 42, wherein said method comprises determining for each of said genes of said first group and for each of said genes of said second group whether a non-wild-type allele is present.

46. A method of screening drug candidates for a potentially useful drug candidate for treating ADHD, said method comprising the steps of:

a) measuring an activity of a wild-type protein selected from the group consisting of TPH, PNMT, ADOA2A, NOS3 and NAT1;

b) measuring an activity of a non-wild-type protein selected from the group consisting of TPH, PNMT, ADOA2A, NOS3 and NAT1, wherein the activity measured in step (b) is the same activity as measured in step (a) and wherein the protein of step (b) is a non-wild-type allele of the protein of step (a);

c) measuring in the presence of a drug candidate an activity of a non-wild-type protein selected from the group consisting of TPH, PNMT, ADOA2A, NOS3 and NAT1, wherein the

activity measured in step (c) is the same as the activity measured in step (a) and wherein the protein of step (c) is a non-wild-type allele of the protein of step (a); and

d) comparing the measured activities of: i) step (a) with step (b) and ii) step (a) with step (c);

wherein if the measured activity of step (c) is closer to the measured activity of step (a) than is the measured activity of step (b) as compared with step (a) then said drug candidate of step (c) is a potentially useful drug candidate for treating ADHD.

47. A method of screening drug candidates for a potentially useful drug candidate for treating ODD, said method comprising the steps of:

a) measuring an activity of a wild-type protein selected from the group consisting of HTR2A, PNMT and CD8;

b) measuring an activity of a non-wild-type protein selected from the group consisting of HTR2A, PNMT and CD8, wherein the activity measured in step (b) is the same activity as measured in step (a) and wherein the protein of step (b) is a non-wild-type allele of the protein of step (a);

c) measuring in the presence of a drug candidate an activity of a non-wild-type protein selected from the group consisting of HTR2A, PNMT and CD8, wherein the activity measured in step (c) is the same as the activity measured in step (a) and wherein the protein of step (c) is a non-wild-type allele of the protein of step (a); and

d) comparing the measured activities of: i) step (a) with step (b) and ii) step (a) with step (c);

wherein if the measured activity of step (c) is closer to the measured activity of step (a) than is the measured activity of step (b) as compared with step (a) then said drug candidate of step (c) is a potentially useful drug candidate for treating ODD.

48. A method of screening drug candidates for a potentially useful drug candidate for treating CD, said method comprising the steps of:

a) measuring an activity of a wild-type protein selected from the group consisting of HTR2A, GABBR1, ADOA2A, GRIN2B, NAT1, CCK, CYP, ESR and CD8;

b) measuring an activity of a non-wild-type protein selected from the group consisting of HTR2A, GABBR1, ADOA2A, GRIN2B, NAT1, CCK, CYP, ESR and CD8, wherein the activity measured in step (b) is the same activity as measured in step (a) and wherein the protein of step (b) is a non-wild-type allele of the protein of step (a);

c) measuring in the presence of a drug candidate an activity of a non-wild-type protein selected from the group consisting of HTR2A, GABBR1, ADOA2A, GRIN2B, NAT1, CCK, CYP, ESR and CD8, wherein the activity measured in step (c) is the same as the activity measured in step (a) and wherein the protein of step (c) is a non-wild-type allele of the protein of step (a); and

d) comparing the measured activities of: i) step (a) with step (b) and ii) step (a) with step (c);

wherein if the measured activity of step (c) is closer to the measured activity of step (a) than is the measured activity of step (b) as compared with step (a) then said drug candidate of step (c) is a potentially useful drug candidate for treating CD.

49. A method of treating a subject for the symptoms of ADHD, said method comprising administering to said subject one or more wild-type genes selected from the group consisting of *TPH*, *PNMT*, *ADOA2A*, *NOS3* and *NAT1*, wherein said one or more wild-type genes are expressed in said subject and further wherein said subject's genome comprises a non-wild-type allele of said one or more wild-type genes which are administered.

50. A method of treating a subject for the symptoms of ODD, said method comprising administering to said subject one or more wild-type genes selected from the group consisting of *HTR2A*, *PNMT* and *CD8*, wherein said one or more wild-type genes are expressed in said subject and further wherein said subject's genome comprises a non-wild-type allele of said one or more wild-type genes which are administered.

51. A method of treating a subject for the symptoms of CD, said method comprising administering to said subject one or more wild-type genes selected from the group consisting of *HTR2A*, *GABBR1*, *ADOA2A*, *GRIN2B*, *NAT1*, *CCK*, *CYP*, *ESR* and *CD8*, wherein said one or

more wild-type genes are expressed in said subject and further wherein said subject's genome comprises a non-wild-type allele of said one or more wild-type genes which are administered.

52. A method of treating a subject for the symptoms of ADHD, said method comprising administering to said subject one or more wild-type proteins selected from the group consisting of TPH, PNMT, ADOA2A, NOS3 and NAT1, wherein said subject's genome comprises a non-wild-type gene encoding an allelic version of said one or more wild-type proteins which are administered.

53. A method of treating a subject for the symptoms of ODD, said method comprising administering to said subject one or more wild-type proteins selected from the group consisting of HTR2A, PNMT and CD8, wherein said subject's genome comprises a non-wild-type gene encoding an allelic version of said one or more wild-type proteins which are administered.

54. A method of treating a subject for the symptoms of CD, said method comprising administering to said subject one or more wild-type proteins selected from the group consisting of HTR2A, GABBR1, ADOA2A, GRIN2B, NAT1, CCK, CYP, ESR and CD8, wherein said subject's genome comprises a non-wild-type gene encoding an allelic version of said one or more wild-type proteins which are administered.